DIFFERENTIAL LABELING FOR QUANTITATIVE ANALYSIS OF COMPLEX PROTEIN MIXTURES

Related Applications

[0001] The present application claims priority to the U.S. Provisional Application Serial No. 60/305,232, filed July 13, 2001, by Haynes, et al., and entitled "DIFFERENTIAL LABELING FOR QUANTITATIVE ANALYSIS OF COMPLEX PROTEIN MIXTURES", and to U.S. Provisional Application Serial No. 60/264,576, filed January 26, 2001, by Haynes, et al., entitled "DIFFERENTIAL LABELING FOR QUANTITATIVE ANALYSIS OF COMPLEX PROTEIN MIXTURES", both of which are incorporated by reference herein in their entirety including any drawings.

Background of the Invention

[0002] Genomic technology has advanced to a point at which, in principle, it has become possible to determine complete genomic sequences and to quantitatively measure the mRNA levels for each gene expressed in a cell. For some species the complete genomic sequence has now been determined, and for one strain of the yeast *Saccharomyces cerevisiae*, the mRNA levels for each expressed gene have been precisely quantified under different growth conditions (Velculescu *et al.*, *Cell* 88:243-251 (1997)). Comparative cDNA array analysis and related technologies have been used to determine induced changes in gene expression at the mRNA level by concurrently monitoring the expression level of a large number of genes (in some cases all the genes) expressed by the investigated cell or tissue (Shalon *et al.*, *Genome Res* 6:639-645 (1996)). Furthermore, biological and computational techniques have been used to correlate specific function with gene sequences. The interpretation of the data obtained by these techniques in the context of the structure, control and mechanism of biological systems has been recognized as a considerable challenge. In particular, it has been extremely difficult to explain the mechanism of biological processes by genomic analysis alone.

[0003] Proteins are essential for the control and execution of virtually every biological process. The rate of synthesis and the half-life of proteins and thus their